AMENDMENTS TO THE SPECIFICATION

Please amend the Specification as follows:

Please amend the section beginning on page 8, line 9 and continuing through line 13 as follows:

The present invention provides isolated nucleic acid molecules, that comprise, or alternatively consist of, a polynucleotide encoding the K+betaM3 protein having the amino acid sequence shown in Figures 1A-B (SEQ ID NO:2) or the amino acid sequence encoded by the cDNA clone, K+betaM3 (also referred to as 2BAC7-D2) deposited as ATCC Deposit Number PTA-4055 ~~XXXXX~~ on February 8, 2002 ~~XXXXX~~.

Please amend Table 1, found on page 41, line 30, as follows:

Gene No.	CDNA CloneID	ATCC Deposit No. Z and Date	Vector	NT SEQ ID. No. X	Total NT Seq of Clone	5' NT of Start Codon of ORF	3' NT of ORF	AA Seq ID No. Y	Total AA of ORF
1.	K+betaM3 (2BAC7-D2)	~~XXXXX Xx/Xx/Xx~~ PTA-4055 2/8/02	Psport1	1	1418	417	1097	2	227

Please amend the Abstract, appearing on page 339, lines 7-14 as follows:

The present invention provides novel polynucleotides encoding K+betaM3 polypeptides, fragments and homologues thereof. Also provided are vectors, host cells, antibodies, and recombinant and synthetic methods for producing K+betaM3 ~~said~~ polypeptides. The invention further relates to diagnostic and therapeutic methods for applying these novel K+betaM3 polypeptides to the diagnosis, treatment, and/or prevention of various diseases and/or disorders related to these polypeptides. The invention further relates to screening methods for identifying agonists and antagonists of the polynucleotides and polypeptides of the present invention.

Please amend the section beginning on page 239, line 16 through line 32 as follows:

Ion channel sequences were used as probes to search the human genomic sequence database. The search program used was gapped BLAST (Altschul et al., 1997). Ion channel specific Hidden Markov Models (HMMs) built in-house or obtained from the public PFAM databases were also used as probes (Bateman et al., 2000). The search program used for HMMs was the Genewise/Wise2

package (http://www.sanger.ac.uk/Software/Wise2/index.shtml). The top genomic exon hits from the results were searched back against the non-redundant protein and patent sequence databases. From this analysis BAC AC012575 was determined to possess a novel ion channel exon based on its homology to the putative human beta subunit K+Hnov28 (SEQ ID NO:6). A predicted exon sequence from BAC AC012575, including 200bp of intron sequence on either side is provided as SEQ ID NO:5. The full length cDNA described herein as K+betaM3 (SEQ ID NO:1, Figures 1A-B), was isolated using probes designed from the BAC AC008652 exon (SEQ ID NO:5). Based on this analysis, a partial sequence of the novel human ion channel related gene, K+betaM3, was identified directly from the genomic sequence. The full-length clone of this novel ion channel gene was experimentally obtained by using the sequence from genomic data.